************ TX REPORT *******

TRANSMISSION OK

TX/RX NO

3225

CONNECTION TEL

912122944700

SUBADDRESS

CONNECTION ID

10/13 15:19

ST. TIME USAGE T

04'53

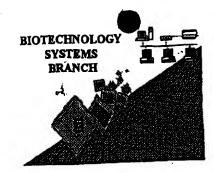
PGS.

12

RESULT

OK

RAW SEQUENCE LIST NG ERROR REPORT



The Biotechnology Systems Branc to of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/ 1134, 583

C/O ALLAN FENUCCI

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLA INSIDET ECTED ERRORS.

PLEASE FORWARD THIS INFORMA IDN TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PI IDITOUT IN YOUR NEXT COMMUNICATION TO THE

APPLICANT, WITH A NOTICE T | (X)MI'LY or, 2) TELEPHONING APPLICANT AN IPAXING A COPY OF THIS PRINTOUT, WITH A

NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS FLICASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRINATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin211 logdu pto.gov or phone 703-306-4119 (R. Wax)

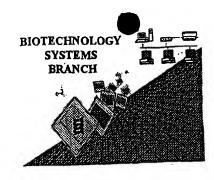
PATENTIN 3.0 e-mail help: patin3ht paus to.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUE (CF. LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACC. SS.BI E THROUGH THE U.S. PATENT AND

TRADEMARK OFFICE WEBSITI SEE BELOW:

Check ar Wersion 3.0

RAW SEQUENCE LISTING ERROR REPORT



FIECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/934,883 C/O // ENUCCE

Date Processed by STIC: 9/6/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Ohecker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ORDOR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/734, S83
ERROR DETECTED	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARI
ATTN: NEW RULES CASES:	
Wrapped Nucleics Wrapped Aminos	The number text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is missligned. Do not use tab codes between numbers; use apace characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
SVariable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220> <223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused fite <220><223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220><223> section to the subsequent amino acid sequence. This applies to the mandatory <220><223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences' (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xsa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220> <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence (
Use of <220>.	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

#E6 OIPE

```
DATE: 09/06/2001
                    RAW SEQUENCE LISTING
                                                             TIME: 15:09:42
                    PATENT APPLICATION: US/09/734,583
                                                                        Does Not Comply
                     Input Set : A:\87534-3000.txt
                                                                    Corrected Diskette Neede
                    Output Set: N:\CRF3\09062001\I734583.raw
      3 <110> APPLICANT: Hornik, Vered
     5 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN
ANALOGS
      7 <130> FILE REFERENCE: 87534-3000
      9 <140> CURRENT APPLICATION NUMBER: 09/734,583
     10 <141> CURRENT FILING DATE: 2000-12-13
     12 <160> NUMBER OF SEQ ID NOS: 10
     14 <170> SOFTWARE: PatentIn version 3.1
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 14
     18 <212> TYPE: PRT
     19 <213> ORGANISM: mammalian
     21 <400> SEQUENCE: 1
     23 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
     27 <210> SEQ ID NO: 2 maked
                                               ) see dene 10 ord 11 on Eval
furnary
     28 <211> LENGTH: 6
     29 <212> TYPE: PRT
C--> 30 <213> ORGANISM: (Artificial peptide
     32 <220> FEATURE:
W--> 33 <221> NAME/KEY: DISULFIDE BRIDGE
        C223> OTHER INFORMATION: Cys residues at amino acid positions and 6 form a disulfide
     34 <222> LOCATION: (1)..(1)
birdg
      39 <220> FEATURE:
      40 <221> NAME/KEY: MOD_RES
      41 <222> LOCATION: (3)..(3)
      42 <223> OTHER INFORMATION: The Trp residue is the D isomer
      45 <400> SEQUENCE: 2
      47 Cys Phe Trp Lys Thr Cys
      48 1
      51 <210> SEQ ID NO: 3
      52 <211> LENGTH: 6
      53 <212> TYPE: PRT/
 C--> 54 <213> ORGANISM( Artificial peptide
      56 <220> FEATURE:
      57 <221> NAME/KEY: MOD_RES
      58 <222> LOCATION: (1)..(1)
      59 <223> OTHER INFORMATION: N-Methyl
      62 <220> FEATURE:
      63 <221> NAME/KEY: MOD_RES
      64 <222> LOCATION: (1)..(6)
      65 <223> OTHER INFORMATION: cyclo
```

69 <221> NAME/KEY: MOD_RES 70 <222> LOCATION: (3)..(3)

71 <223> OTHER INFORMATION: The Trp residue is the D isomer

68 <220> FEATURE:

74 <400> SEQUENCE: 3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001 TIME: 15:09:42

Input Set : A:\87534-3000.txt

Output Set: N:\CRF3\09062001\I734583.raw

```
76 Ala Tyr Trp Lys Val Phe
     77 1
     80 <210> SEQ ID NO: 4
     81 <211> LENGTH: 8
     82 <212> TYPE: PRT
C--> 83 <213> ORGANISM: (Artificial Peptide
     85 <220> FEATURE:
     86 <221> NAME/KEY: MOD RES
     87 <222> LOCATION: (1)..(1)
     88 <223> OTHER INFORMATION: The Phe residue is a D isomer
     91 <220> FEATURE:
     92 <221> NAME/KEY: MOD_RES
     93 <222> LOCATION: (8)..(8)
     94 <223> OTHER INFORMATION: The Thr residue ends with CH2OH
     97 <220> FEATURE:
                                                    bridge
W--> 98 <221> NAME/KEY: DISULFIDE BRIDGE
     100 <223> OTHER INFORMATION: A disulfide (bride) is formed between Cys residues 2 and 7
                                              Cys is at breation 2
      103 <220> FEATURE:
      104 <221> NAME/KEY: MOD_RES
      105 <222> LOCATION (2)..(2) T. Cys is CAT APC
106 <223> OTHER INFORMATION: The Trp residue is a D isomer
      109 <400> SEQUENCE: 4
      111 Phe Cys Phe Trp Lys Thr Cys Thr
      112 1'
      115 <210> SEQ ID NO: 5
      116 <211> LENGTH: 7
      117 <212> TYPE: PRT
 C--> 118 <213> ORGANISM: (Artificial Peptide
      120 <220> FEATURE:
 W--> 121 <221> NAME/KEY: DISULFIDE
      123 <223> OTHER INFORMATION: A Disulfide Bridge is formed between the Cys residues at
 position
                 2 and 6
       124
      127 <220> FEATURE:
      128 <221> NAME/KEY: MOD_RES
       129 <222> LOCATION: (1)..(1)
      130 <223> OTHER INFORMATION: The Phe residue is a D isomer
       133 <220> FEATURE:
       134 <221> NAME/KEY: MOD_RES
       135 <222> LOCATION: (4)..(4)
       136 <223> OTHER INFORMATION: The Trp residue is a D isomer
       139 <220> FEATURE:
                                             residue
       140 <221> NAME/KEY: MOD_RES
       141 <222> LOCATION: (7)...(7)
       142 <223> OTHER INFORMATION: The Thr (residue) ends with N2H
       145 <400> SEQUENCE: 5
       147 Phe Cys Phe Trp Lys Cys Thr
                , 5 ,
       148 1
```

DATE: 09/06/2001

TIME: 15:09:42

```
Input Set : A:\87534-3000.txt
                    Output Set: N:\CRF3\09062001\I734583.raw
    151 <210> SEQ ID NO: 6
     152 <211> LENGTH: 8
     153 <212> TYPE: PRT
C--> 154 <213> ORGANISM: Artificial peptide
     156 <220> FEATURE:
     157 <221> NAME/KEY: MISC_FEATURE
     159 <223> OTHER INFORMATION: is a gamma amino butyric acid, diamino butyric acid, Gly,
                  5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bi bridged
beta-Al
              rdged to Residue 8; Residue 1 also begins with a hydrogen, or a m
     160
     161
               ono- or di- saccharide attached
     162
     165 <220> FEATURE:
     166 <221> NAME/KEY: MISC_FEATURE
     167 <222> LOCATION: (2)..(2)
     168 <223> OTHER INFORMATION: is (D) or (L) Phe or Tyr
     171 <220> FEATURE:
     172 <221> NAME/KEY: MISC_FEATURE
     174 <223> OTHER INFORMATION: is (D) or (L)-Trp, or (L)-Phe, (D)- or (L)-INal or (D) or
                1, or Tyr
      175
      178 <220> FEATURE:
      179 <221> NAME/KEY: MISC_FEATURE
      180 <222> LOCATION: (4)..(4)
      181 <223> OTHER INFORMATION: is (D) or (L)-Trp
      184 <220> FEATURE:
      185 <221> NAME/KEY: MISC_FEATURE
      186 <222> LOCATION: (5)..(5)
      187 <223> OTHER INFORMATION: is (D) or (L)-Lys
      190 <220> FEATURE:
      191 <221> NAME/KEY: MISC_FEATURE
      193 <223> OTHER INFORMATION: is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or
  (L)-A
                la, or Tyr
      194
      197 <220> FEATURE:
      198 <221> NAME/KEY: MISC_FEATURE
       200 <223> OTHER INFORMATION: is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;
       203 <220> FEATURE:
       204 <221> NAME/KEY: MISC_FEATURE
       206 <223> OTHER INFORMATION: is Gly, Val, Leu, (D) or (L)-Phe, or 1Nal or 2Nal; with a
                 l carboxy acid, amide or alcohol group.
  termina
       207
                              ( (
       210 <4,00> SEQUENCE; 6_
  W--> 212 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                         , 5
       213 1
       216 <210> SEQ ID NO: 7
       217 <211> LENGTH: 7
       218 <212> TYPE: PRT
  C--> 219 <213> ORGANISM Artificial Peptide
```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/734,583

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001 TIME: 15:09:42

Input Set : A:\87534-3000.txt

Output Set: N:\CRF3\09062001\1734583.raw

```
221 <220> FEATURE:
     222 <221> NAME/KEY: MISC_FEATURE
     223 <222> LOCATION: (1)..(1)
     224 <223> OTHER INFORMATION: is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is
brid
               ged to Residue 6 a bridging group composed of 1 to 5 methyl space
               rs connected to an amide, thioether, thioester, or disulfide, fol
     226
               lowed by 1 to 5 methyl spacers .
     230 <220> FEATURE:
     231 <221> NAME/KEY: MISC_FEATURE
     232 <222> LOCATION: (2)..(2)
     233 <223> OTHER INFORMATION: is Tyr or (D) - or (L)-Phe
     236 <220> FEATURE:
     237 <221> NAME/KEY: MISC FEATURE
     238 <222> LOCATION: (3)..(3)
     239 <223> OTHER INFORMATION: is (D) - or (L) -Trp, (D) - or (L) -1Nal, or (D) - or (L) -2Nal
     242 <220> FEATURE:
     243 <221> NAME/KEY: MISC_FEATURE
     244 <222> LOCATION: (5)..(5)
     245 <223> OTHER INFORMATION: is Thr, Val, Ser, or Cys
     248 <220> FEATURE:
     249 <221> NAME/KEY: MISC_FEATURE
     250 <222> LOCATION: (6)..(6)
     251 <223> OTHER INFORMATION: is Gly or (D) - or (L) -Phe
     254 <220> FEATURE:
      255 <221> NAME/KEY: MISC_FEATURE
     257 <223> OTHER INFORMATION: is Thr, GABA, (D) - or (L)-1Nal, (D) - or (L)-2Nal, or (D) - or
 (L
               ) -Phe
      258
      261 <4,00> SEQUENCE: 7
W--> 263 Xaa Xaa Xaa Lys Xaa Xaa Xaa
                                                                     see den Son Error
funnan
She
wardle begil invalid
      264 1
      267 <210> SEQ ID NO: '8
      268 <211> LENGTH: 9
      269 <212> TYPE: PRT/
 C--> 270 <213> ORGANISM( Artificial Peptide
      272 <220> FEATURE:
      273 <221> NAME/KEY: MISC FEATURE
      274 <222> LOCATION: (1)..(1)
      275 <223> OTHER INFORMATION: is absent or is a terminal group of one to four amino acids
      278 <220> FEATURE:
      279 <221> NAME/KEY: MISC_FEATURE
      280 <222> LOCATION: (2)..(2)
      281 <223> OTHER INFORMATION: is 1Nal, 2Nal, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or
 (D
                ) - or (L) -Phe
      285 <220> FEATURE:
      286 <221> NAME/KEY: MISC FEATURE
      287 <222> LOCATION: (3)..(4)
      288 <223> OTHER INFORMATION: may be absent, or are independently Gly, Tyr, 1Nal, 2Nal,
 Beta-As
                 p (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe
```

DATE: 09/06/2001

TIME: 15:09:42

```
Input Set : A:\87534-3000.txt
                    Output Set: N:\CRF3\09062001\I734583.raw
    292 <220> FEATURE:
    293 <221> NAME/KEY: MISC_FEATURE
    294 <222> LOCATION: (5)..(5)
    295 <223> OTHER INFORMATION: (D) - or (L)-Trp
    298 <220> FEATURE:
    299 <221> NAME/KEY: MISC_FEATURE
    300 <222> LOCATION: (6)..(6)
    301 <223> OTHER INFORMATION: (D) - or (L)-Lys
    304 <220> FEATURE:
    305 <221> NAME/KEY: MISC_FEATURE
    307 <223> OTHER INFORMATION: is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or
(D)
               - or (L)-Phe
    308
    311 <220> FEATURE:
    312 <221> NAME/KEY: MISC_FEATURE
     313 <222> LOCATION: (8)..(8)
     314 <223> OTHER INFORMATION: is Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe
     317 <220> FEATURE:
     318 <221> NAME/KEY: MISC_FEATURE
     319 <222> LOCATION: (9)..(9)
     320 <223> OTHER INFORMATION: is absent or is Val, Thr, 1Nal or 2Nal
     323 /400> SEQUENCE: 8
W--> 325/Xaa) Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     326
     329 <210> SEQ ID NO: 9
     330 <211> LENGTH: 7
     331 <212> TYPE: PRT
C--> 332 <213> ORGANISM: (Artificial Peptide
     334 <220> FEATURE:
     335 <221> NAME/KEY: MISC_FEATURE
     337 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is
                to Residue 7 by a bridge comprised of 1 to 5 methylene spacers (co) Cohnected
connected
               incected to an amide, thioether, thioester, or disulfide, followe
      338
      339
                d by 1 to 5 methylene spacers
      343 <220> FEATURE:
      344 <221> NAME/KEY: MISC_FEATURE
      346 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
      345 <222> LOCATION: (2)..(2)
      349 <220> FEATURE:
      350 <221> NAME/KEY: MISC_FEATURE
      352 <223> OTHER INFORMATION: is absent or is (D) - or (L) -Phe, Tyr or (D) - or (L) -Ala;
      355 <220> FEATURE:
      356 <221> NAME/KEY: MISC FEATURE
      357 <222> LOCATION: (4)..(4)
      358 <223> OTHER INFORMATION: is (D) - or (L) Tyr
      361 <220> FEATURE:
       362 <221> NAME/KEY: MISC_FEATURE
                                        Use of n and/or Xaa has been detected in the Sequence Listing.
```

Use of n and/or Xaa has been detected in the Sequence Listing Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/734,583

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001 TIME: 15:09:43

Input Set : A:\87534-3000.txt

Output Set: N:\CRF3\09062001\I734583.raw

L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2 L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2 L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3 L:83 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4 L:98 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4 L:118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5 L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5 L:154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6 L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 L:219 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7 L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 L:270 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8 L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 L:332 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9 L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 L:388 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10 L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10



SERIAL NUMBER	FILING DATE		FIRST NAME	D APPLICANT	ATTORNEY DOCKET NO.
			1		EXAMINER
				ART UNIT	PAPER NUMBER
			1	DATE MAILED:	

Please find below a communication from the EXAMINER in charge of this application Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for 1. nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF-could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Apariation No.: 09 734,583

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

	1.	This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
	2.	This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
	3.	A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
	4.	A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
X	5.	The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	6.	The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
	7.	Other:
□ Ap.		icant Must Provide:
_	pl	
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X X X	pl A A in A a 1.	icant Must Provide: In initial or substitute computer readable form (CRF) copy of the "Sequence Listing". In initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry ito the specification. It is statement that the content of the paper and computer readable copies are the same and, where policable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or

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Examiner Anish Gupta

GAU 1653



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Day: Wednesday Date: 10/13/2004 Time: 16:48:14

Application Number Information

Application Number: 09/734583 Assignments

Filing Date: 12/13/2000

Effective Date: 12/13/2000

Application Received: 12/13/2000

Pat. Num./Pub. Num: /20020052315

Issue Date: 00/00/0000

Date of Abandonment: 00/00/0000

Attorney Docket Number: 87534-3000

Third Level Review: NO Status: 94 / PUBLICATIONS -- ISSUE FEE PAID - NOT MATCHED WITH

FILE

Confirmation Number: 3691

Oral Hearing: NO

Group Art Unit: 1654

Interference Number:

Unmatched Petition: NO

<u>L&R Code</u>: Secrecy Code:1

Lost Case: NO

Class/Subclass: 514/009.000

Title of Invention: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN

Examiner Number: 79808 / AUDET, MAURY

IFW IMAGE

Query Request

Secrecy Order: NO

Status Date: 08/12/2004

Mail N/=.

Waiting for Response Desc.

ANALOGS

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Appln Contents Petition Info	Atty/Agent Info	Continuity Data	Foreign Data Inventors	A A
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PCT //	Search	or PG PUBS#	Search	
Attorney Docket #		Search		
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Content Information for 09/734583

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Date	Status	Code	Description		
09/08/2004		QURI	WORKFLOW - QUERY REQUEST - BEGIN (18 BAD Zonda Park		
08/12/2004	94	IFEE	ISSUE FEE PAYMENT RECORDED		
06/11/2004	93	R1021	RECEIPT INTO PUBS		
06/08/2004		SENT	WORKFLOW - FILE SENT TO CONTRACTOR		
05/19/2004	92	MN/=.	MAIL NOTICE OF ALLOWANCE		
05/17/2004		IREV	ISSUE REVISION COMPLETED		
05/17/2004	90	N/=.	NOTICE OF ALLOWANCE DATA VERIFICATION COMPLETED		
05/17/2004	89	CNTA	NOTICE OF ALLOWABILITY		
03/04/2004		TDP	TERMINAL DISCLAIMER FEE PAID		
03/04/2004		FWDX	DATE FORWARDED TO EXAMINER		
02/23/2004	71	A	RESPONSE AFTER NON-FINAL ACTION		
02/23/2004		XT/G	REQUEST FOR EXTENSION OF TIME - GRANTED		
10/08/2003		M844	INFORMATION DISCLOSURE STATEMENT (IDS) FILED		
09/23/2003	41	MCTNF	MAIL NON-FINAL REJECTION		
09/22/2003	40	CTNF	NON-FINAL REJECTION		
03/04/2003		DOCK	CASE DOCKETED TO EXAMINER IN GAU		
10/04/2002		DOCK	CASE DOCKETED TO EXAMINER IN GAU		
09/20/2001		CRFD	CRF IS FLAWED TECHNICALLY / NOT ENTERED INTO DATABASE		
09/08/2001		PA	CHANGE IN POWER OF ATTORNEY (MAY INCLUDE ASSOCIATE P		
09/08/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE		
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08/20/2001		A.PE	PRELIMINARY AMENDMENT		
08/20/2001		A.PE	PRELIMINARY AMENDMENT		
07/05/2001	30	DOCK	CASE DOCKETED TO EXAMINER IN GAU		
06/29/2001	20	OIPE	APPLICATION DISPATCHED FROM OIPE		
06/29/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE		
05/29/2001		SCAN	IFW SCAN & PACR AUTO SECURITY REVIEW		
01/24/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE		